

AFTER HIS KIND:
THE BIOLOGICAL UNIT OF CREATION

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DESIGN IN NATURE

Design in nature has been a topic of debate for centuries. We have no intention of trying to argue conclusively on a philosophic basis that it is intelligent design. Rather, we hope to show briefly by example that the need for intelligence in bringing about the various designs in nature is by no means a preposterous proposition. We maintain that there are two recognizable yet intuitively distinct forms of design, that which is easily explainable in terms of physical properties and processes and that which requires intelligent ordering. Some contrasting examples will make the point. When a water droplet freezes around a dust particle, an elaborately designed snowflake results, simply due to physical properties. The same is true for the development of a crystal in a supersaturated solution. Just let the solution cool and then tap it. Order suddenly emerges as the crystal develops. In the American West, there are numerous examples of natural sculpture. Chimneys, arches, bridges, human profiles, etc., all dutifully sketched from the rock by the forces of wind and rain. But one would not confuse such structures with Mt. Rushmore, or the Golden Gate Bridge, or the World Trade Center. These human architectural artifacts show clearly the marks of intelligent design. The sharp geometrical forms and the finely sculpted lines are recognized intuitively as the works of human intelligence. The simple point is that intelligent design is discernably different from natural design.

Carl Sagan uses the same reasoning in telling of the search for intelligent life on Mars. Initially, the canals on Mars, as visible through telescopes, were thought to be possible evidences of intelligent life. Because of the patterns involved, it was possible the canals were engineered by intelligent beings. However, upon closer inspection, first by space probes passing close by, and eventually by actually landing on Mars, the canals faded into nothingness, superficial artifacts and nothing more. However, as one approaches Earth, the conclusion is the opposite. From the distances of space there is nothing about Earth's surface which betrays the presence of intelligence. There are continents and seas with no observable patterns. But as one gets closer and sharpens the focus, geometry is revealed in the forms of farms and fields, highways, streets, and buildings. Suddenly the presence of intelligence is unmistakable.

With living things, the best of both perspectives is readily apparent. From a distance, biological organisms are indeed marvelously adapted to their environments. They slither, crawl, walk, run, fly, and some go nowhere at all. If we can be excused for speaking anthropomorphically, there is beauty, humor, mystery, and drama. But what happens upon closer scrutiny? Does the apparent design fade into nothingness? On the contrary, it explodes into a maze of integrated complexity. Not only do geometrical patterns reemerge in microscopic form as in the feather of a bird or the scales of a butterfly wing, but at the molecular level, volumes are needed to express all that goes on. Orchestrating the whole process is the genetic machinery operating through the DNA blueprint. The mark of intelligence is unmistakable.

This brings us to the topic of information theory. Though there will be more on this later, suffice it to say at this time, that information codes, of which DNA is one, require intelligent manipulation, not only to create the vocabulary, but also to set up the rules of transmission. For our purposes, the analogy can follow this way. Suppose you were walking down the beach or a river bank and, as one would expect, you observe ripples in the sand. A perfect example of natural order due to the physical properties of the sand and water and the movement of water in waves over the sand. Easily explainable. But let us say you decide to walk further. Later, you come across the

words "JOHN LOVES MARY" written in the sand. We intuitively recognize this as intelligent manipulation of matter to formulate coded information. In DNA there are precise symbols or letters (nucleotides) grouped into words (codons). These words are also arranged in a particular sequence to form sentences (genes) or complete thoughts. To go further, sentences are strung together to form paragraphs (regulatory groups or operons) and paragraphs are set in order to form chapters (chromosomes) and volumes (genomes).

By simply applying some basic criteria to living systems, the evidence of intelligent design is overwhelming, if not compelling. We believe that the application of information theory to the field of genetics will yield a comprehensible theory of limited biological change. We attempt here to present a model of limited biological change constrained by the genetic machinery yet endowed with an impressive display of variability and hence adaptability. This is essentially the creationist's concept of the created kind. Various attempts have been made to suggest theories for delineating the boundaries of a kind. Marsh's theory of gametic fusion states that only organisms within a kind will produce a successful fusion of sperms and eggs with varying degrees of success following zygote formation. But this approach is rather simplistic and offers no rationale for why this is so. Another suggestion is based on behavioral similarities. Two problems surface here. First, it will only apply to animals, and second, it still does not deal with the mechanism. What causes these behaviors to be different? If there is so much room for variation, how can the kinds retain their integrity? It is our intention to propose a creationist model of limited biological change based on the genetic structure of organisms.

GENETICS AND INFORMATION THEORY

In recent years, several authors have exposed the connection between the genetic code of DNA and information theory. These studies, for the most part, have concerned themselves specifically with the origins of the genetic code. The overwhelming conclusion is that information does not and cannot arise spontaneously by mechanistic processes. Intelligence is a necessity in the origin of an informational code, including the genetic code, no matter how much time is given. The old analogy of sitting a monkey at a typewriter, and given enough time, he would produce the complete works of Shakespeare, is foolish. On a computer, William Bennett set one trillion monkeys to typewriters, typing ten keys a second at random. We would have to wait a trillion times the estimated age of the universe before we would even see the sentence, "To be, or not to be: that is the question." It may be statistically possible for a pot of water to freeze when placed on a stove burner, but the real probability is so absurd it is hardly worth talking about. The same is true of monkeys typewriting Shakespeare.

But that is not our problem. Our concern is what happens after the code is in place. Similar to language, there are two fundamental principles involved in the expression of genetic information. First, there is a finite set of words which are the essentials of content. In organisms, this is comparable to structural genes. Second, there are the rules of grammar which provide for the richness of expression using the finite set of words. In organisms, these rules or programs consist of the regulatory mechanisms. In human language, given a finite set of words and a single set of rules, variety of expression becomes virtually limitless. In fact, in information theory, the more interesting question is not, "What does this message say?", but "Why was this expression of a thought chosen over the countless others which could have done the job?" This concept could provide the basis for a model of extensive variability based on slightly different genes (alleles) within the same set of rules or regulatory mechanisms. The power of recombination can take on a whole new meaning.

This could also provide the clue as to what mechanism preserves the integrity of a created kind. It can be shown that what separates the higher taxonomic categories are perhaps the regulatory mechanisms and not just structural genes. It is conceivable, therefore, that the different kinds are characterized by slightly different regulatory mechanisms, different programs. Certainly there are structural genes present in a mouse which are not to be found in a bacterium; but these structural gene differences would probably distinguish only major categories such as Phylum and Class. Structural gene differences within the mammals may be much more subtle. We are not talking here about mere amino acid sequence differences, but whole genes, structural information found in one organism but not present in another. However, by a simple change of rules, wholly new expressions are made possible, also rich in variety. The regulatory mechanisms would both constrain and provide for variety simultaneously. The created kinds, therefore, maintain their integrity in the face of a vast array of variation by virtue of their own unique set of regulatory mechanisms.

On the other hand, one might say that if language is so powerful in its ability to produce variety and novelty, couldn't mutation and natural selection change the rules of regulatory mechanisms to produce biological novelty? The answer lies in the origin of life question. Informational codes are constructed of vocabulary and grammar. Both, of necessity, are produced only by intelligence. Random changes in letter and word sequences ultimately can produce only gibberish. The same will result if one attempts to change the rules.

According to evolution, the primary vehicle for the addition of new information is gene duplication. Subsequent mutations to the new redundant gene then produce a new gene. Since the new redundant gene is free from selection pressures, it can mutate rather freely. Of course, most of these sequences would degenerate into gibberish, mere genetic noise, but it is hoped that they will eventually mutate to a useful form.

This hope flies in the face of all that we know of the origin of informational codes. Words do not descend to gibberish by random changes only to ascend back to a new meaning by the same process. As biologists, we also wonder how the redundant gene slips out of the selective process only to slip back in once the new meaningful gene is complete. Was the copied gene no longer translated into protein while mutating? And if so, how was it included back into the process later on?

The initial rules of genetic grammar did not arise by chance. Additional rules did not result from random modifications of the existing rules. The information and programs which distinguish the kinds have their origin in the intelligence of their Creator. With structural genes, gene duplication only produces genes of similar function; nothing new emerges. Duplication of regulatory genes can only arrive at the same end. This, we believe, will be supported further by the advances and application of information theory to the field of genetics.

Admittedly, this proposal at present is highly theoretical. We offer it, not as a final answer, but as potential framework for scientific investigation. Undoubtedly, there will be the need for extensive refinements. After all, our understanding of regulatory mechanisms is still on the ground floor. Indeed, some would say we haven't even finished laying the foundation yet. But it is a start. We may even be wrong. But that is the nature of science, and admittedly, as creationists, we have been far too timid to stick our necks out. It is time to openly bring forth constructive ideas which will lead to fruitful research. It is our sincere hope that this is one.

THE CREATED KIND: A DEFINITION

At the outset, many might complain that the concept of a created kind is not a legitimate scientific pursuit because its origin is from the Bible. The word "kind" is a biblical term from which we do not want to hide. However, many theories of science have had their origin from stranger sources. Kekule gained his inspiration for the chemical ring structure from a dream of a snake biting its tail. Tesla got the idea for the alternating current motor from a vision while reading the poet Goethe. The point is that one's source for an idea is irrelevant. The key is whether the theory is practical and testable. If our theory of the created kind is to be rejected, let it be for a lack of scientific integrity, and not that its inspiration is biblical.

To help alleviate any bias that may arise from the use of the phrase "created kind", we have proposed the word "prototype" in its place. "Proto" being the Latin prefix meaning "ancestral" and "type" deriving from the latin word meaning "image". This provides a Latin base consistent with the rest of taxonomy while providing for the essential meaning of an ancestral image or form upon which numerous variations are possible.

It is admittedly not an easy task to submit a definition of a prototype which has significant biological meaning. In taxonomy, this difficulty is not without precedent. There is no universal agreement over what a species is, let alone whether there are two, three, or five kingdoms. In evolutionary taxonomy, all organisms are said to be related through descent. Therefore the species is the only category that has any objective criteria, that of reproductive isolation from other species. Unfortunately, one cannot always determine whether two populations are reproductively isolated or not. There are degrees of isolation which make even species designations tenuous. But, at least, in many cases reproductive isolation is a testable entity. Not so for categories from Genus on up to Kingdom. These distinctions are based primarily upon degrees of similarity and dissimilarity. All objectivity soon vanishes. With the inclusion of prototype, a new,

frequently testable taxonomic category is introduced.

For taxonomic purposes, a prototype could be simply defined as "all organisms that are descended from a single created population". This definition necessitates the making of two distinctions. First, the prototype is not synonymous with species. To speak of the fixity of species is outdated and inaccurate. A prototype may consist of only one species, or it may be comprised of dozens of species. Some groups, due to organismal and ecological characteristics, speciate more readily than others. This concept would hold true under the banner of prototypes as well. Secondly, the prototype cannot be universally associated with any particular taxonomic level. Evolutionists who demand identification of the created kind with some particular taxon betray their own ignorance of the subjectivity of higher taxonomic levels. In some groups, it may turn out to be synonymous with family, and in others, with genera or even species. The prototype is a discrete objective unit; therefore, it will not be useful to attempt broad identification with any one taxonomic unit across the board.

This makes the identification of the prototype more difficult. This may prove to be a monumental task for creationary biologists. The identification of the prototypes becomes a process of reevaluation according to traditional and non-traditional methods:

1. Morphology. The structure or appearance of organisms has been the predominant method of distinguishing taxonomic categories since Linnaeus, the father of taxonomy. This would still make a useful initial step. A woodpecker is not an ostrich, and a rose is not a dandelion. The current taxonomic levels of Kingdom, Phylum, and Class would still be most helpful at this point.

2. Embryology. Where this may prove helpful is in beginning to determine the role of regulatory mechanisms in embryonic development. This could also be carried over into post-natal development. Fundamental differences here may lead to distinguishing characters in terms of the regulatory structure.

3. Chromosome morphology. Since differences in gross chromosome morphology usually are the cause of hybrid sterility, it follows that chromosome morphology may help in identifying members of a particular prototype, as well as excluding others. It is interesting to note that in 1977, a standardized chromosome set was proposed for the North American deer mouse (*Peromyscus*) which includes more than 50 species. With all of the species studied, the consistent element is chromosome number ($2n=48$). Among the various species, considerable variation is seen in the way the chromosomes are organized, but it seems obvious that these are all related species within one prototype. The next step would be to compare chromosome morphology with other genera with similar organismal morphologies, such as the house mouse (*Mus*).

4. Structural genes. This would not only involve amino acid sequence differences of protein, such as cytochrome C which is common to most organisms, but also delineation of proteins unique to certain groups. This is one area about which we know very little at present, but which holds a great deal of potential, if we are applying information theory correctly.

5. Regulatory mechanisms. This is undoubtedly the critical area of investigation of the future. We know so little about it. We have a fairly good concept of the relationship between a single structural gene and its protein product. Our knowledge of the relationship between the gene and the organism as a whole is virtually nil.

Much of this mystery undoubtedly is caught up in the regulatory mechanisms.

6. A host of other biological facts could also serve as additional criteria. These would include behavior, physiology, reproductive patterns, and success or failure of gametic fusion. In short, in many cases it will require a very extensive knowledge of the organism to make the identification. At times various levels of data may seem to conflict. An illustrative example is that of humans and the great apes. Anatomically and behaviorally, man is quite distinct from the orangutan, gorilla, and chimpanzee. However, genic and highly detailed chromosome studies show an unexpectedly high degree of similarity.

To summarize our concept of the prototype, let us emphasize that a host of biological techniques may be applicable in identifying the members of a kind, as well as distinguishing between the prototypes. No one criterion such as chromosome morphology, behavior, gametic fusion, etc. will be definitive in all cases. At times, a single test may be sufficient; at others, a multiplicity of approaches will be necessary. However, in terms of the mechanism of limited variation, the application of information theory to

the genetic machinery should prove the most promising. The crucial factor will be delineation of the necessity of intelligent design in the structuring of the informational content and grammar of the genome of each prototype. This will indicate not only the necessity of intelligence in originating the genetic code in the broad universal sense, but also in the specific sense of the unique adaptive programs of each prototype. But just as a word of caution, it is necessary to point out that although the prototype has an objective reality, we may only be able to hypothesize about a particular organism's inclusion in a prototype. The taxonomic ambiguity of the giant panda would be a problem for the creationist as well as the evolutionist.